

SEQUENCE LISTING

<110> GOITSUKA, Ryo

<120> A mast cell-specific adapter molecules and cDNAs thereof

<130> 2003-1609/WMC/00653

<140> NEW

<141> 2003-11-21

<150> PCT/JP00/06351

<151> 2000-9-17

<150> JP11-263778

<151> 1999-09-17

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

<211> 1721

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (255)..(1562)

<300>

<301> Goitsuka R., et al.

<302> A BASH/SLP-76-related adaptor protein MIST/Clink involved in IgE receptor-mediated mast cell degranuation

<303> Int. Immunol.

<304> 12

<305> 4

<306> 573-580

<307> 2000

<308> GenBank/AB021220

<309> 2000-05-26

<400> 1

acgaggccaa actgcccagg tctgtggctg cgtttctcg 60
acatacaagg cactctctgc tgaaggactc tgctgagggg 120
cttacagagt gctccagat ggcaccgtgg accccccttc 180
actgagccct tgactaaagg aagactgagc aggctgagtt 240
aggtgccaag gacc atg acc agc cag ggc aat aaa 290
Met Thr Ser Gln Gly Asn Lys Arg Thr Thr Lys Glu
1 5 10

gga ttc ggt gat ctg aga ttc cag aac gtc tct ctg 338
Gly Phe Gly Asp Leu Arg Phe Gln Asn Val Ser Leu Leu Lys Asn Arg
15 20 25

tca tgg cca agc ctc agc agt gcc aaa ggg cgg 386
Ser Trp Pro Ser Leu Ser Ser Ala Lys Gly Arg Cys Arg Ala Val Leu
30 35 40

gaa cca ctt ccg gat cac aga agg aac ttg gct 434
Glu Pro Leu Pro Asp His Arg Arg Asn Leu Ala Gly Val Pro Gly Gly
45 50 55 60

gaa aaa tgc aac agt aac aac gac tac gaa gat 482
Glu Lys Cys Asn Ser Asn Asn Asp Tyr Glu Asp Pro Glu Phe Gln Leu
65 70 75

ctg aag gca tgg cca tca atg aaa att tta cca gcc 530
Leu Lys Ala Trp Pro Ser Met Lys Ile Leu Pro Ala Arg Pro Ile Gln
80 85 90

gaa tcg gaa tac gca gat aca cgc tat ttc cag gat atg atg gag gct	578
Glu Ser Glu Tyr Ala Asp Thr Arg Tyr Phe Gln Asp Met Met Glu Ala	
95 100 105	
ccc ctt ctg tta cct ccc aag gct tct gtc tcc act gag aga caa acc	626
Pro Leu Leu Leu Pro Pro Lys Ala Ser Val Ser Thr Glu Arg Gln Thr	
110 115 120	
agg gat gtg agg atg aca cag ctg gaa gaa gtg gac aag cct acc ttc	674
Arg Asp Val Arg Met Thr Gln Leu Glu Val Asp Lys Pro Thr Phe	
125 130 135 140	
aag gat gtc aga agc caa cgc ttt aaa gga ttc aaa tac aca aaa ata	722
Lys Asp Val Arg Ser Gln Arg Phe Lys Gly Phe Lys Tyr Thr Lys Ile	
145 150 155	
aac aag act cct ttg cca cct cct cgg cct gct atc act ctc ccc aag	770
Asn Lys Thr Pro Leu Pro Pro Arg Pro Ala Ile Thr Leu Pro Lys	
160 165 170	
aag tac caa ccc tta ccc cca gca cca cca gag gag agc agt gca tac	818
Lys Tyr Gln Pro Leu Pro Pro Ala Pro Pro Glu Glu Ser Ser Ala Tyr	
175 180 185	
ttc gct cca aag ccc acc ttt cca gaa gtc cag agg ggg ccc agg cag	866
Phe Ala Pro Lys Pro Thr Phe Pro Glu Val Gln Arg Gly Pro Arg Gln	
190 195 200	
agg agt gca aaa gac ttc agt agg gtc ctt gga gca gaa gaa gaa tct	914
Arg Ser Ala Lys Asp Phe Ser Arg Val Leu Gly Ala Glu Glu Glu Ser	
205 210 215 220	
cac cac cag aca aag cca gaa tct tct tgc cca tca tca aac caa aac	962
His His Gln Thr Lys Pro Glu Ser Ser Cys Pro Ser Ser Asn Gln Asn	
225 230 235	
aca cag aag agt cca cct gcc att gcc agc tct tcc tac atg cca gga	1010
Thr Gln Lys Ser Pro Pro Ala Ile Ala Ser Ser Ser Tyr Met Pro Gly	
240 245 250	
aag cac agt ata caa gcc aga gac cat aca ggt agc atg cag cac tgt	1058
Lys His Ser Ile Gln Ala Arg Asp His Thr Gly Ser Met Gln His Cys	
255 260 265	
cct gct cag aga tgc caa gct gca gcc agc cac agc cct cga atg ctg	1106
Pro Ala Gln Arg Cys Gln Ala Ala Ala Ser His Ser Pro Arg Met Leu	
270 275 280	
ccc tat gaa aac aca aac tcg gag aaa cct gac ccc aca aag cct gat	1154
Pro Tyr Glu Asn Thr Asn Ser Glu Lys Pro Asp Pro Thr Lys Pro Asp	
285 290 295 300	
gag aag gat gtc tgg cag aat gaa tgg tac att gga gaa tac agt cgc	1202
Glu Lys Asp Val Trp Gln Asn Glu Trp Tyr Ile Gly Glu Tyr Ser Arg	
305 310 315	
cag gca gtg gaa gat gtg tta atg aaa gag aac aag gat ggt act ttt	1250
Gln Ala Val Glu Asp Val Leu Met Lys Glu Asn Lys Asp Gly Thr Phe	
320 325 330	
ttg gtc cga gac tgc tct aca aaa tcc aag gca gaa cca tat gtt ttg	1298
Leu Val Arg Asp Cys Ser Thr Lys Ser Lys Ala Glu Pro Tyr Val Leu	
335 340 345	
gtg gtg ttt tat ggg aac aag gtc tac aat gtg aaa atc cgt ttc ctc	1346
Val Val Phe Tyr Gly Asn Lys Val Tyr Asn Val Lys Ile Arg Phe Leu	
350 355 360	
gag agc aat caa cag ttt gcc ctg ggc aca gga cta cga gga aat gag	1394
Glu Ser Asn Gln Gln Phe Ala Leu Gly Thr Gly Leu Arg Gly Asn Glu	
365 370 375 380	
atg ttt gat tct gtg gaa gac atc att gaa cac tac aca tat ttt ccc	1442
Met Phe Asp Ser Val Glu Asp Ile Ile Glu His Tyr Thr Tyr Phe Pro	
385 390 395	
att ctg cta ata gat ggg aaa gac aag gct gca cgc agg aaa cag tgc	1490
Ile Leu Leu Ile Asp Gly Lys Asp Lys Ala Ala Arg Arg Lys Gln Cys	
400 405 410	
tac ctc acc cag cca ctg cct ctc gcc agg ctc ctt ctc act cag tac	1538
Tyr Leu Thr Gln Pro Leu Pro Leu Ala Arg Leu Leu Leu Thr Gln Tyr	
415 420 425	
tcc agc cag gca ctt cat gag taa gaagcccagc cagatatccc cgcatcagtg	1592

Ser Ser Gln Ala Leu His Glu
430 435

gcctggccct tgtctcattc ctggctcaat ggattcagtt cttcttccat ctgcatttat 1652
ctgcaaagta ttatttctg tgtcttcaag ggatgattt ttgactctgt aaaaaaaaaa 1712
aaaaaaaaaa 1721

<210> 2
<211> 435
<212> PRT
<213> Mus musculus

<400> 2
Met Thr Ser Gln Gly Asn Lys Arg Thr Thr Lys Glu Gly Phe Gly Asp
1 5 10 15
Leu Arg Phe Gln Asn Val Ser Leu Leu Lys Asn Arg Ser Trp Pro Ser
20 25 30
Leu Ser Ser Ala Lys Gly Arg Cys Arg Ala Val Leu Glu Pro Leu Pro
35 40 45
Asp His Arg Arg Asn Leu Ala Gly Val Pro Gly Gly Glu Lys Cys Asn
50 55 60
Ser Asn Asn Asp Tyr Glu Asp Pro Glu Phe Gln Leu Leu Lys Ala Trp
65 70 75 80
Pro Ser Met Lys Ile Leu Pro Ala Arg Pro Ile Gln Glu Ser Glu Tyr
85 90 95
Ala Asp Thr Arg Tyr Phe Gln Asp Met Met Glu Ala Pro Leu Leu Leu
100 105 110
Pro Pro Lys Ala Ser Val Ser Thr Glu Arg Gln Thr Arg Asp Val Arg
115 120 125
Met Thr Gln Leu Glu Glu Val Asp Lys Pro Thr Phe Lys Asp Val Arg
130 135 140
Ser Gln Arg Phe Lys Gly Phe Lys Tyr Thr Lys Ile Asn Lys Thr Pro
145 150 155 160
Leu Pro Pro Pro Arg Pro Ala Ile Thr Leu Pro Lys Lys Tyr Gln Pro
165 170 175
Leu Pro Pro Ala Pro Pro Glu Glu Ser Ser Ala Tyr Phe Ala Pro Lys
180 185 190
Pro Thr Phe Pro Glu Val Gln Arg Gly Pro Arg Gln Arg Ser Ala Lys
195 200 205
Asp Phe Ser Arg Val Leu Gly Ala Glu Glu Ser His His Gln Thr
210 215 220
Lys Pro Glu Ser Ser Cys Pro Ser Ser Asn Gln Asn Thr Gln Lys Ser
225 230 235 240
Pro Pro Ala Ile Ala Ser Ser Ser Tyr Met Pro Gly Lys His Ser Ile
245 250 255
Gln Ala Arg Asp His Thr Gly Ser Met Gln His Cys Pro Ala Gln Arg
260 265 270
Cys Gln Ala Ala Ala Ser His Ser Pro Arg Met Leu Pro Tyr Glu Asn
275 280 285
Thr Asn Ser Glu Lys Pro Asp Pro Thr Lys Pro Asp Glu Lys Asp Val
290 295 300
Trp Gln Asn Glu Trp Tyr Ile Gly Glu Tyr Ser Arg Gln Ala Val Glu
305 310 315 320
Asp Val Leu Met Lys Glu Asn Lys Asp Gly Thr Phe Leu Val Arg Asp
325 330 335
Cys Ser Thr Lys Ser Lys Ala Glu Pro Tyr Val Leu Val Val Phe Tyr
340 345 350
Gly Asn Lys Val Tyr Asn Val Lys Ile Arg Phe Leu Glu Ser Asn Gln
355 360 365
Gln Phe Ala Leu Gly Thr Gly Leu Arg Gly Asn Glu Met Phe Asp Ser
370 375 380
Val Glu Asp Ile Ile Glu His Tyr Thr Tyr Phe Pro Ile Leu Leu Ile
385 390 395 400
Asp Gly Lys Asp Lys Ala Ala Arg Arg Lys Gln Cys Tyr Leu Thr Gln

<210> 3
<211> 1814
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (241)..(1527)

<300> GenBank/AB110420
<308> 2003-05-22
<309> (1)..(1814)
<313>

<400> 3 ggctgcattt cacaggaaac caagtctaaa acggacctat caggagggtt tctgctgaag ggcactgctt agcatcgaga agaattcaac ccaccgcctt actaatttcc agtgcccaa ggtctctgca ctgccgcccc tcctcacagg agacggacac ctcagcctag atcccttgg gctctccacg ctgttcaggc tgaattgaag agccctctta cccgccaggt gccaagaact atg aac agg cag ggc aat aga aag aca act aaa gaa gga tcc aac gat Met Asn Arg Gln Gly Asn Arg Lys Thr Thr Lys Glu Gly Ser Asn Asp 1 5 10 15 ttg aaa ttc cag aac ttc agt ctg cca aaa aac agg tca tgg cct cgc Leu Lys Phe Gln Asn Phe Ser Leu Pro Lys Asn Arg Ser Trp Pro Arg 20 25 30 atc aat agt gcc aca ggc cag tac cag agg atg aac aag cct ctt cta Ile Asn Ser Ala Thr Gly Gln Tyr Gln Arg Met Asn Lys Pro Leu Leu 35 40 45 gac tgg gaa aga aac ttt gct gca gtc ctg gat gga gca aaa ggc cac Asp Trp Glu Arg Asn Phe Ala Ala Val Leu Asp Gly Ala Lys Gly His 50 55 60 agt gat gat gac tat gat gac cct gag ctt cggt atg gaa gag aca tgg Ser Asp Asp Asp Tyr Asp Asp Pro Glu Leu Arg Met Glu Glu Thr Trp 65 70 75 80 cag tcg att aaa att tta cca gcc cggt cct ata aag gaa tct gaa tat Gln Ser Ile Lys Ile Leu Pro Ala Arg Pro Ile Lys Glu Ser Glu Tyr 85 90 95 gca gat aca cac tat ttc aag gtt gca atg gac act ccc ctt ccg tta Ala Asp Thr His Tyr Phe Lys Val Ala Met Asp Thr Pro Leu Pro Leu 100 105 110 gac acc agg acc tct atc tcc att gga cag ccg acc tgg aac aca cag Asp Thr Arg Thr Ser Ile Ser Ile Gly Gln Pro Thr Trp Asn Thr Gln 115 120 125 acg agg ttg gaa aga gtg gac aaa ccc att tcc agg gac gtc aga agc Thr Arg Leu Glu Arg Val Asp Lys Pro Ile Ser Arg Asp Val Arg Ser 130 135 140 caa aac att aaa gga gat gca tcc gta aga aag aac aag att cct tta Gln Asn Ile Lys Gly Asp Ala Ser Val Arg Lys Asn Lys Ile Pro Leu 145 150 155 160 cca cct cct cgg cct ctc ata aca ctt ccg aag aag tac caa ccc ttg Pro Pro Pro Arg Pro Leu Ile Thr Leu Pro Lys Lys Tyr Gln Pro Leu 165 170 175 ccc cct gag ccg gag agc agc agg cca cct tta tct cag aga cac acc Pro Pro Glu Pro Glu Ser Ser Arg Pro Pro Leu Ser Gln Arg His Thr 180 185 190 ttt cca gaa gtc cag gga atg ccc agt cag ata agc tta agg gac tta Phe Pro Glu Val Gln Gly Met Pro Ser Gln Ile Ser Leu Arg Asp Leu 195 200 205	60 120 180 240 288 336 384 432 480 528 576 624 672 720 768 816 864
--	--

195	200	205	
agt gag gtc ctt gaa gca gaa	aaa gtt cct cat aac cag agg aag cct		
Ser Glu Val Leu Glu Ala Glu	Lys Val Pro His Asn Gln Arg Lys Pro		912
210	215	220	
gaa tca act cat ctg tta gaa aac caa aat act caa gag att cca ctt			960
Glu Ser Thr His Leu Leu Glu Asn Gln Asn	Thr Gln Glu Ile Pro Leu		
225	230	235	240
gcc att agc agt tct tca ttc acg aca agc aac cac agt gtg caa aac			1008
Ala Ile Ser Ser Ser Phe Thr Thr Ser Asn His Ser Val Gln Asn			
245	250	255	
aga gat cat aga gga ggc atg cag ccc tgt tct cct cag aga tgc cag			1056
Arg Asp His Arg Gly Gly Met Gln Pro Cys Ser Pro Gln Arg Cys Gln			
260	265	270	
cct cca gcc agc tgc agc cct cac gaa aat ata ctg ccc tat aaa tac			1104
Pro Pro Ala Ser Cys Ser Pro His Glu Asn Ile Leu Pro Tyr Lys Tyr			
275	280	285	
aca agc tgg aga cca cct ttc ccc aaa agg tct gat aga aag gat gtc			1152
Thr Ser Trp Arg Pro Pro Phe Pro Lys Arg Ser Asp Arg Lys Asp Val			
290	295	300	
cag cac aat gaa tgg tac att gga gaa tac agc cgc cag gca gtg gaa			1200
Gln His Asn Glu Trp Tyr Ile Gly Glu Tyr Ser Arg Gln Ala Val Glu			
305	310	315	320
gag gca ttc atg aag gag aac aag gat ggt agt ttc ttg gtc cga gat			1248
Glu Ala Phe Met Lys Glu Asn Lys Asp Gly Ser Phe Leu Val Arg Asp			
325	330	335	
tgt tcc aca aaa tcc aag gaa gag ccc tat gtt ttg gct gtg ttt tat			1296
Cys Ser Thr Lys Ser Lys Glu Glu Pro Tyr Val Leu Ala Val Phe Tyr			
340	345	350	
gag aac aaa gtc tac aat gta aaa atc cgc ttc ctg gag agg aat cag			1344
Glu Asn Lys Val Tyr Asn Val Lys Ile Arg Phe Leu Glu Arg Asn Gln			
355	360	365	
cag ttt gcc ctg ggg aca gga ctc aga gga gat gag aag ttt gat tca			1392
Gln Phe Ala Leu Gly Thr Gly Leu Arg Gly Asp Glu Lys Phe Asp Ser			
370	375	380	
gta gaa gac atc atc gaa cac tac aag aat ttt ccc att ata cta att			1440
Val Glu Asp Ile Ile Glu His Tyr Lys Asn Phe Pro Ile Ile Leu Ile			
385	390	395	400
gat ggg aaa gat aaa act ggg gtc cac agg aaa cag tgt cac ctc act			1488
Asp Gly Lys Asp Lys Thr Gly Val His Arg Lys Gln Cys His Leu Thr			
405	410	415	
cag cca ctc cct ctc acc aga cac ctc ttg cct ctg tag cctggcttt			1537
Gln Pro Leu Pro Leu Thr Arg His Leu Leu Pro Leu			
420	425		
gtgttatctt tggtttactg gattcagcgc ttccattgtt ttcatgtt tcaaaagttt			1597
atttctgtg cctcaaggg acaactttt taactttgga gaaaagaaaa acactctata			1657
acagagagtg gaaaatact cacggttttg aaagttcaaa ccacagagaa aatatttata			1717
acatgcaaaa aataaaaaaca tttctagtaa ctggccactg gaaaataaat aaaaataaaa			1777
actaaaaaaaaa aagaaaaaaaaa aaaaaaaaaa aaaaaaaaaa			1814

<210> 4
<211> 428
<212> PRT
<213> Homo sapiens

<400> 4

Met Asn Arg Gln Gly Asn Arg Lys Thr Thr Lys Glu Gly Ser Asn Asp
1 5 10 15
Leu Lys Phe Gln Asn Phe Ser Leu Pro Lys Asn Arg Ser Trp Pro Arg
20 25 30
Ile Asn Ser Ala Thr Gly Gln Tyr Gln Arg Met Asn Lys Pro Leu Leu
35 40 45
Asp Trp Glu Arg Asn Phe Ala Ala Val Leu Asp Gly Ala Lys Gly His

50	55	60
Ser Asp Asp Asp Tyr Asp Asp Pro Glu Leu Arg Met Glu Glu Thr Trp	70	75
65		80
Gln Ser Ile Lys Ile Leu Pro Ala Arg Pro Ile Lys Glu Ser Glu Tyr	85	90
		95
Ala Asp Thr His Tyr Phe Lys Val Ala Met Asp Thr Pro Leu Pro Leu	100	105
		110
Asp Thr Arg Thr Ser Ile Ser Ile Gly Gln Pro Thr Trp Asn Thr Gln	115	120
		125
Thr Arg Leu Glu Arg Val Asp Lys Pro Ile Ser Arg Asp Val Arg Ser	130	135
		140
Gln Asn Ile Lys Gly Asp Ala Ser Val Arg Lys Asn Lys Ile Pro Leu	145	150
		155
Pro Pro Pro Arg Pro Leu Ile Thr Leu Pro Lys Lys Tyr Gln Pro Leu	165	170
		175
Pro Pro Glu Pro Glu Ser Ser Arg Pro Pro Leu Ser Gln Arg His Thr	180	185
		190
Phe Pro Glu Val Gln Gly Met Pro Ser Gln Ile Ser Leu Arg Asp Leu	195	200
		205
Ser Glu Val Leu Glu Ala Glu Lys Val Pro His Asn Gln Arg Lys Pro	210	215
		220
Glu Ser Thr His Leu Leu Glu Asn Gln Asn Thr Gln Glu Ile Pro Leu	225	230
		235
Ala Ile Ser Ser Ser Phe Thr Thr Ser Asn His Ser Val Gln Asn	245	250
		255
Arg Asp His Arg Gly Gly Met Gln Pro Cys Ser Pro Gln Arg Cys Gln	260	265
		270
Pro Pro Ala Ser Cys Ser Pro His Glu Asn Ile Leu Pro Tyr Lys Tyr	275	280
		285
Thr Ser Trp Arg Pro Pro Phe Pro Lys Arg Ser Asp Arg Lys Asp Val	290	295
		300
Gln His Asn Glu Trp Tyr Ile Gly Glu Tyr Ser Arg Gln Ala Val Glu	305	310
		315
Glu Ala Phe Met Lys Glu Asn Lys Asp Gly Ser Phe Leu Val Arg Asp	325	330
		335
Cys Ser Thr Lys Ser Lys Glu Glu Pro Tyr Val Leu Ala Val Phe Tyr	340	345
		350
Glu Asn Lys Val Tyr Asn Val Lys Ile Arg Phe Leu Glu Arg Asn Gln	355	360
		365
Gln Phe Ala Leu Gly Thr Gly Leu Arg Gly Asp Glu Lys Phe Asp Ser	370	375
		380
Val Glu Asp Ile Ile Glu His Tyr Lys Asn Phe Pro Ile Ile Leu Ile	385	390
		395
Asp Gly Lys Asp Lys Thr Gly Val His Arg Lys Gln Cys His Leu Thr	405	410
		415
Gln Pro Leu Pro Leu Thr Arg His Leu Leu Pro Leu	420	425